

Raw Sequence Listing Error Summary

ERROR DETECTEDSUGGESTED CORRECTION

SERIAL NUMBER: 091534,861B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
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- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☒ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/534,861B

DATE: 11/17/03

TIME: 10:40:58

S. W. O. P. 5

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4      Ebskamp, Michael
5      Geerts, Hendrikis
6      Weisbeek, Petrus
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13 <141> CURRENT FILING DATE: 2000-03-24
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46 Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu Pro Ser Asp Ala
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50 Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser Ala Cys Ala Thr
51      25      30      35
53 atg ctg acc gcc tgg gcc atg ggg gtg gtc gtc gtc ggc gcc acc ctg      201
54 Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val Gly Ala Thr Leu
55      40      45      50
57 atg ggg gac tgg acc atg ggg gac gac gac gac gac gac gac gac gac      249
58 Leu Ala Gly Leu Ala Met Ala Ala Ala Val Arg Ala Ala Ala Ala Ala
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/534,861B

DATE: 11-17-2003

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127 gaa aac aac tgg tgg tgg ttc atg ttt tat gtt ttt tat gtt ttt ttt      1114
128 Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly Glu Val Asp Ser
129      360      365      370
130 aag cgg gct gat gtc gtc aag gga tgg gct tcc att cag tca gtt cct      1209
131 Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile Gln Ser Val Pro
132      375      380      385
133 agg aag gtg gct ctg gat gag aag acc cgg aag aac ctg ctg ctg tgg      1257
134 Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp
135      390      395      400
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137 Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala Thr Glu Leu Thr
138      405      410      415      420
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140 Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile Pro Leu Arg Gln
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144      440      445      450
145 gcc gtg gct gcc ctg aac gag gcc gat gtg gcc tac aac tgc agt agc      1449
146 Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser
147      455      460      465
148 agc gcc gcc gct gtt aac cgc gcc gcc cta gcc ccc ttc gcc ctg ctg      1497
149 Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu
150      470      475      480
151 gtc ctg gcc gcc ggt gac cgc cgt gcc gag caa aag gcc gtc tac ttc      1545
152 Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr Ala Val Tyr Phe
153      485      490      495      500
154 tac gtg tct agg gcc ctt gac gga gcc ctg cac acc agc ttc tgc caa      1593
155 Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr Ser Phe Cys Gln
156      505      510      515
157 gat gag ctg aga tgg tca cga gcc aag gat gtg acc aag cgt gtc atc      1641
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159      520      525      530
160 ggg agc acg gtg ccg gtg ctg gac ggt gag gct ttg tca atg agg gtg      1689
161 Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu Ser Met Arg Val
162      535      540      545
163 ctg gtg gat cac tcc atc gtg cag gcc ttc gac atg gcc ggg agg acc      1737
164 Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met Gly Gly Arg Thr
165      550      555      560
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167 Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr Gln Glu Ala Arg
168      565      570      575      580
169 gtc tac ttg ttc aac aac gcc acc ggt gcc agc gtg aag gcc gaa agg      1833
170 Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val Thr Ala Glu Arg
171      585      590      595
172 ctg gtt ttt cac ttt atc cag ttt ttt cag ttt cag ttt cag ttt ttt      1881

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Figure 1: Schematic representation of the experimental design. The diagram shows a sequence of events: 'Presentation of the stimulus' (a box with a question mark), 'Response' (a box with a question mark), 'Feedback' (a box with a question mark), and 'Inter-trial interval' (a box with a question mark). The sequence is repeated for 'Trial 1' and 'Trial 2'. The 'Response' box is labeled 'Correct' or 'Incorrect'. The 'Feedback' box is labeled 'Correct' or 'Incorrect'. The 'Inter-trial interval' box is labeled 'Correct' or 'Incorrect'.

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213	<400>	SEQUENCE: 2														
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216	1			5						10					15	
219	Pro	Ser	Asp	Ala	Ala	Asp	Gly	Lys	Arg	Thr	Gly	Cys	Met	Arg	Trp	Ser
220			20						25					30		
223	Ala	Cys	Ala	Thr	Val	Leu	Thr	Ala	Ser	Ala	Met	Ala	Val	Val	Val	Val
224			35					40					45			
227	Gly	Ala	Thr	Leu	Leu	Ala	Gly	Leu	Arg	Met	Glu	Gln	Ala	Val	Asp	Glu
228			50				55					60				
231	Glu	Ala	Ala	Ala	Gly	Gly	Phe	Pro	Trp	Ser	Asn	Glu	Met	Leu	Gln	Trp
232	65					70					75				80	
235	Gln	Arg	Ser	Gly	Tyr	His	Phe	Gln	Thr	Ala	Lys	Asn	Tyr	Met	Ser	Asp
236				85						90				95		
239	Pro	Asn	Gly	Leu	Met	Tyr	Tyr	Arg	Gly	Trp	Tyr	His	Met	Phe	Tyr	Gln
240				100					105					110		
243	Tyr	Asn	Pro	Val	Gly	Thr	Asp	Trp	Asp	Asp	Gly	Met	Glu	Trp	Gly	His
244			115					120					125			
247	Ala	Val	Ser	Arg	Asn	Leu	Val	Gln	Trp	Arg	Thr	Leu	Pro	Ile	Ala	Met
248			130					135				140				
251	Val	Ala	Asp	Gln	Trp	Tyr	Asp	Ile	Leu	Gly	Val	Leu	Ser	Gly	Ser	Met
252	145					150					155				160	
255	Thr	Val	Leu	Pro	Asn	Gly	Thr	Val	Ile	Met	Ile	Tyr	Thr	Gly	Ala	Thr
256					165					170					175	
259	Asn	Ala	Ser	Ala	Val	Glu	Val	Gln	Cys	Ile	Ala	Thr	Pro	Ala	Asp	Pro
260				180					185					190		
263	Asn	Asp	Pro	Leu	Leu	Arg	Arg	Trp	Thr	Lys	His	Pro	Ala	Asn	Pro	Val
264				195				200					205			
267	Ile	Trp	Ser	Pro	Pro	Gly	Val	Gly	Thr	Lys						

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/534,861B

DATE: 11/17/03

TIME: 1:14:17

Input File: A:\15313SEQrev.txt

Output File: N:\CRF4\01172003\I534861B.raw

```

377 Gly Arg Arg Ser Ser Asp Asn Ser Val Glu Met Leu His Val Leu Lys
378 385 395
391 Ala Ser Met Asp Asp Glu Arg His Arg Tyr Tyr Ser Leu Val Thr Tyr
392 395 405
395 Asp Ser Ala Ala Asn Thr Thr Thr Pro Ile Asp Pro Glu Leu Asp Leu
396 398 400 402 404
399 Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser
399 400 402 404 406
403 Phe Tyr Asp Pro Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly
404 406 408 410 412
407 Glu Val Asp Ser Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile
408 410 412 414
411 Gln Ser Val Pro Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn
412 414 416 418 420
415 Leu Leu Leu Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala
416 418 420 422 424
419 Thr Glu Leu Thr Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile
420 422 424 426 428
423 Pro Leu Arg Gln Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His
424 426 428 430 432
427 Leu Asp Ala Ser Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr
428 430 432 434 436
431 Asn Cys Ser Ser Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro
432 434 436 438 440
435 Phe Gly Leu Leu Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr
436 438 440 442 444
439 Ala Val Tyr Phe Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr
440 442 444 446 448
443 Ser Phe Cys Gln Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr
444 446 448 450 452
447 Lys Arg Val Ile Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu
448 450 452 454 456
451 Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met
452 454 456 458 460
455 Gly Gly Arg Thr Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr
456 458 460 462 464
459 Gln Glu Ala Arg Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val
460 462 464 466 468
463 Thr Ala Glu Arg Leu Val Val His Glu Met Asp Ser Ala His Asn Gln
464 466 468 470 472
467 Leu Ser Asn Glu Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser
468 470 472 474 476
371 Arg His
372 625
375 <210> SEQ ID NO: 3
376 <211> LENGTH: 30
377 <212> TYPE: PNA
378 <213> ORGANISM: Synthesia PNA
379 <214> ORIGIN: 1

```

inserted residue, see error summary sheet
item 10

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/534,861B

DATE: 01/17/2003
TIME: 10:40:14

Input Seq : A:\15313SEQrev.txt
Output Seq: N:\CRF4\01172003\I534861B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 6,12,18

Seq#:12; Xaa Pos. 5,7,8,11,13

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/534,861B

DATE: 1/17/03

TIME: 1:46:14

Input File: A:\15313SEQrev.txt

Output File: N:\CRF4\01172003\1534861B.raw

1:12 M:11 C: Current Application Number differs, Replaced Current Application Number

1:47 M:41 W: 4 "a" or "Xia" used, for SP, ID=11 added: s.1

1:47 M:41 W: 4 "a" or "Xia" used, for SP, ID=11 added: s.1